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Fig. 1

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Fig. 2







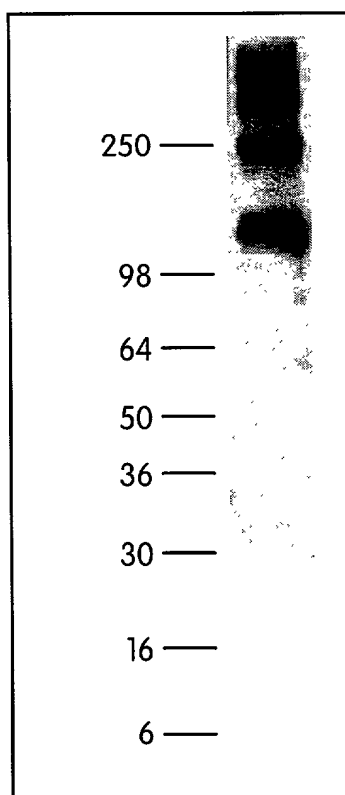


Fig. 5

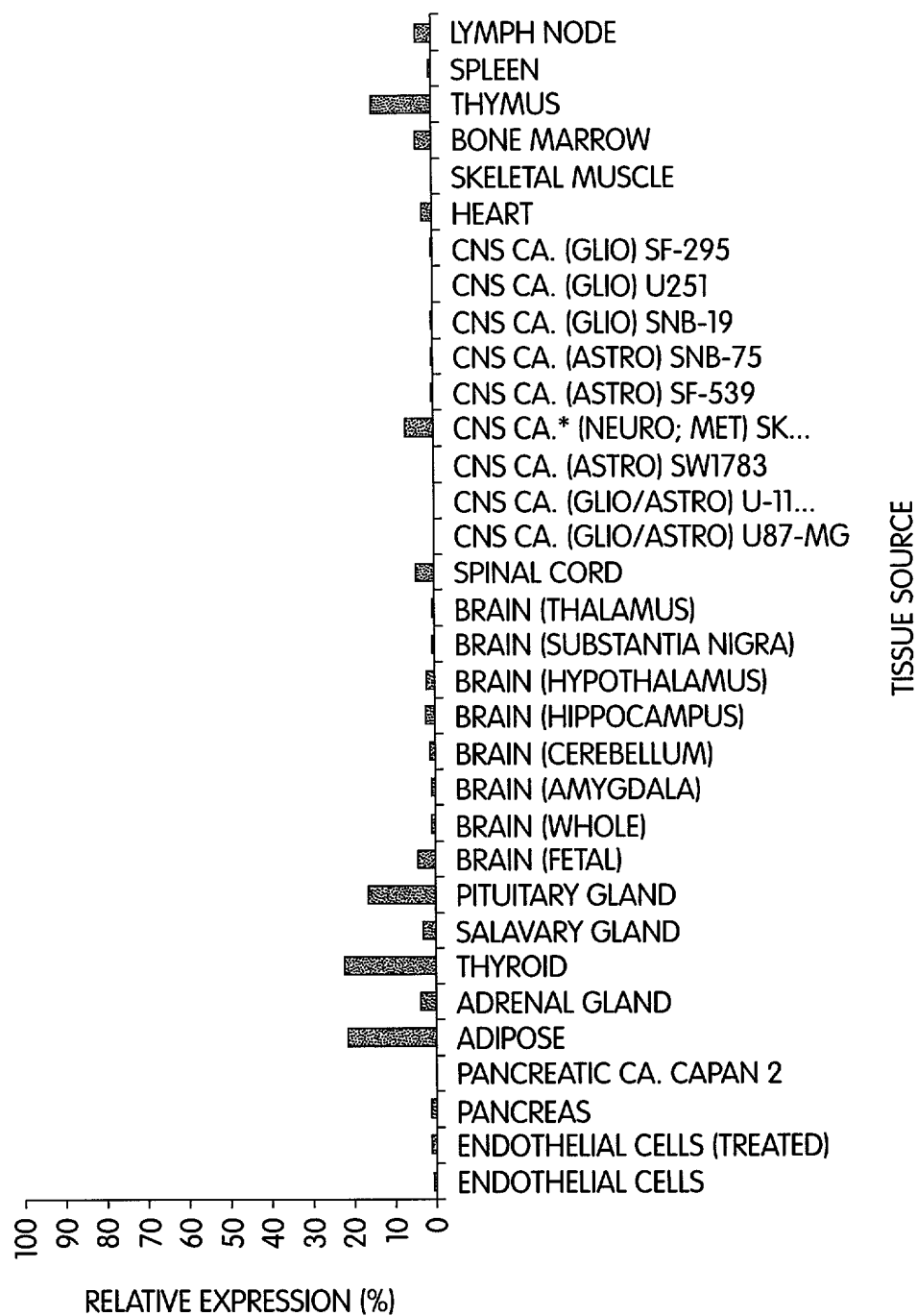
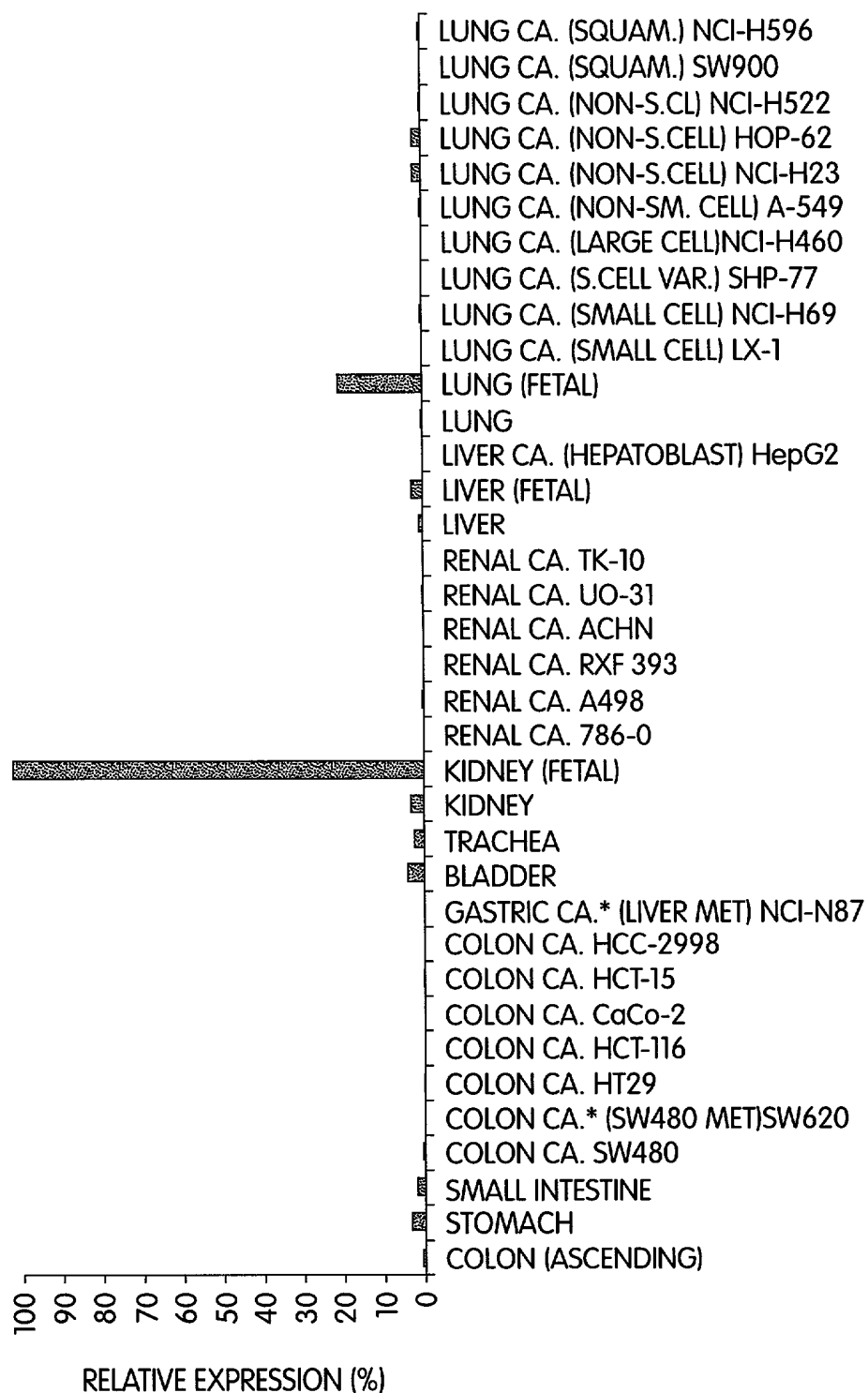
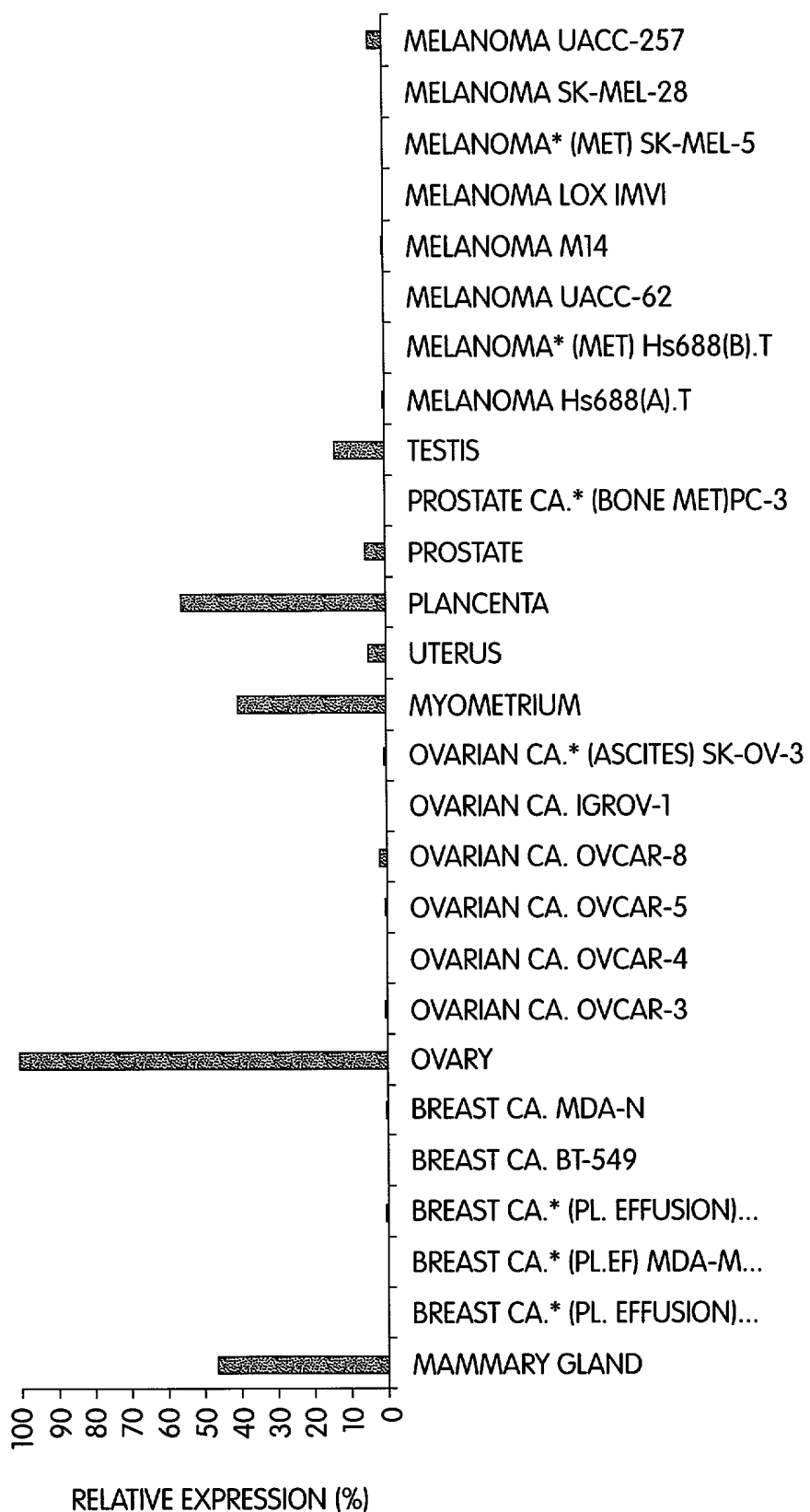


Fig. 6A



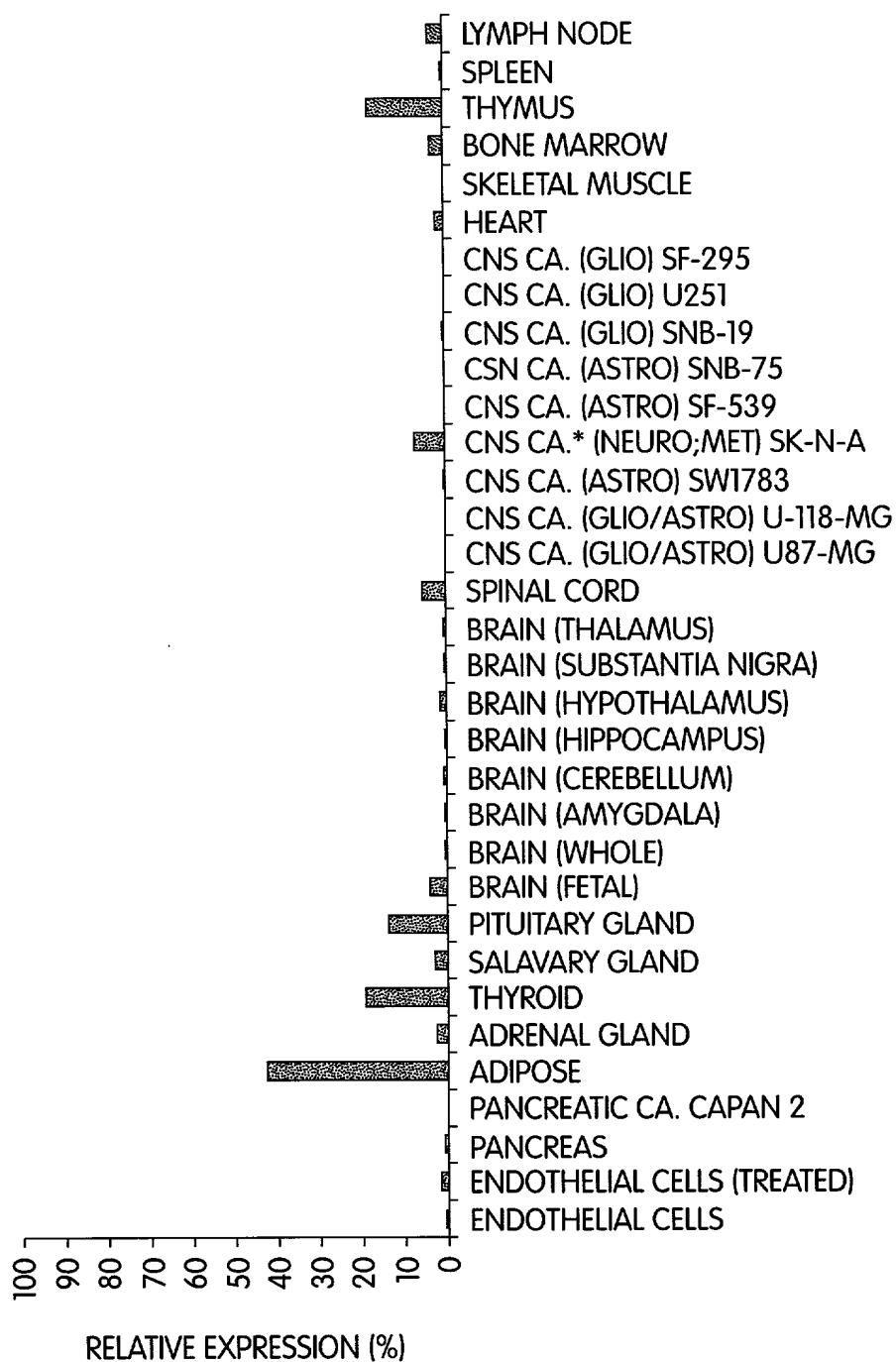
TISSUE SOURCE

Fig. 6B



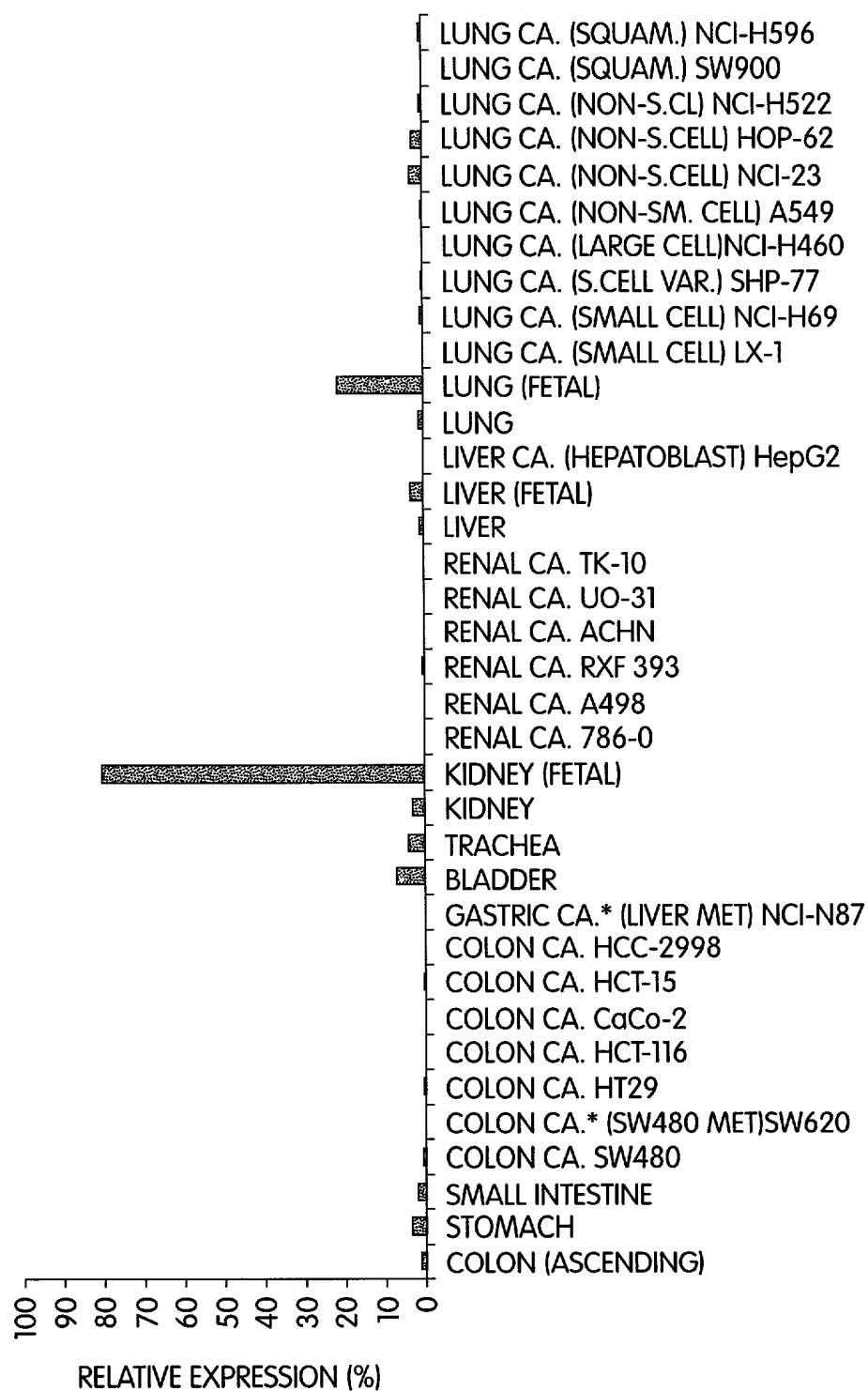
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Fig. 6C



TISSUE SOURCE

Fig. 7A



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Fig. 7B

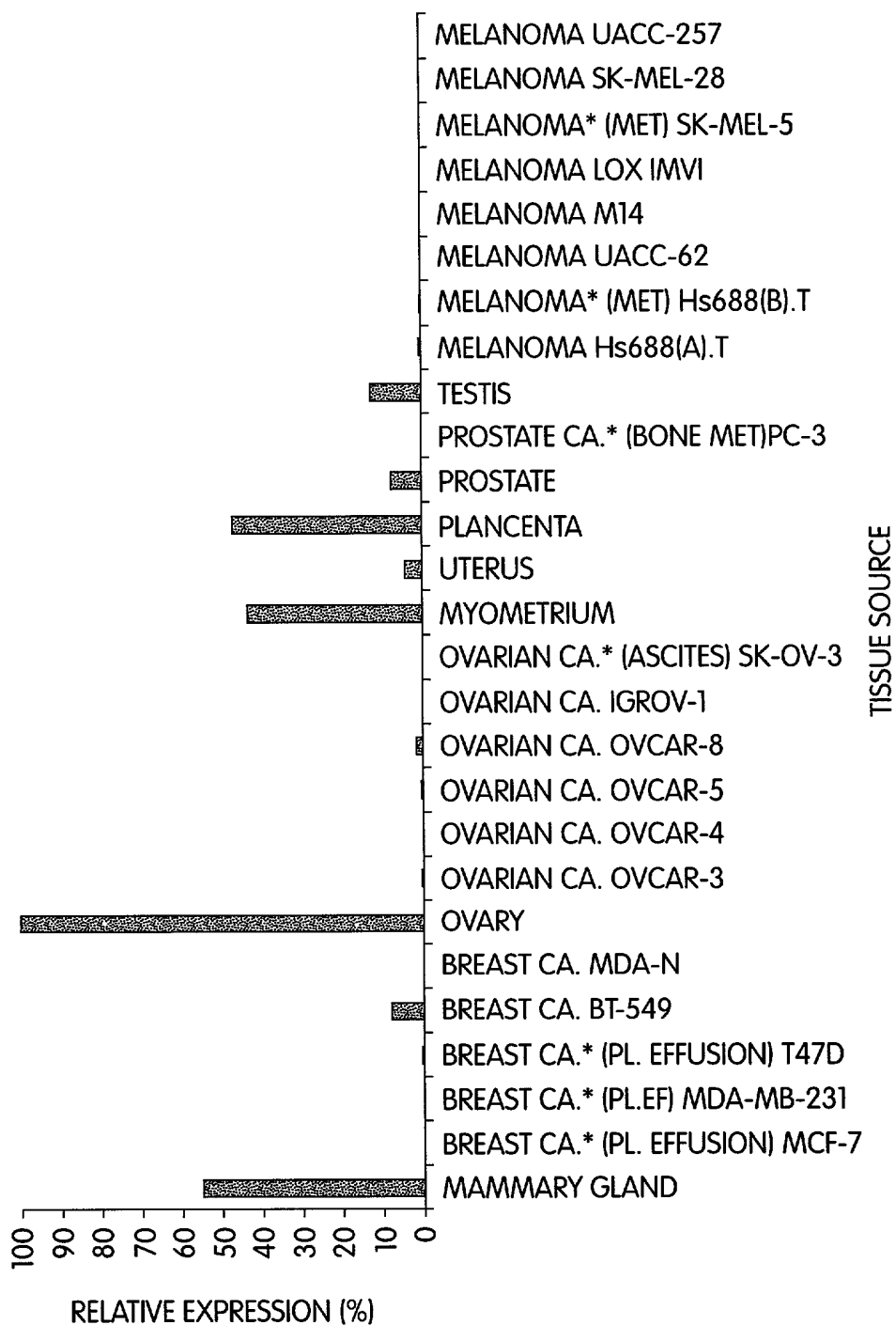


Fig. 7C

Figure 8

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CTTGGCCAGAACTGTGAGTTGCCAACGAGAACTCAAGCTGGTTCACTGGCAGTCCGAAA  
ACAGAAAAGAGCCCTGGCCAGTCCCTCACCCCTAAGGGCAAGGACAGCCAGGTATCCCTT  
CTCTAGGGCTTCAAGATCCACAGAAGAGCTGCCTCCACCGGGACCGGCAGTTCCCCAAA  
GAGTAAAGAACCAGACCGTGGAAGGAAGCAGAGAGAAAAAGGAAGAGGGAAATCCCAGTG  
AAGTCCCCGTATGGGCCACCAAGATGCCAGGCGAGGTGTGAGAGCTCCGGAACCGGGAAG  
TGTTTGGCTCCCGGGTGGTAAAGAAGCTTATCAACAACCGTGTAGGTCTGAAAAGGAAAG  
TTTTATTAGACGGAAGGACGAGGCAGCAGAGCGCAGTAGGCGCTTCAAGCAAGAGAGGAC  
TGAGCTCCCTGCGGGGAAGTGCAGGGTAATTTGGACCACATTAGTCACTTAGGTGATGGT  
AAATGGTTACATTTGTGATATTTTGGTGCCTTGATGTCAGCAAAGTTTGCACAATGGGT  
CTTAACGTGCACTCATTCGGGAAACGTACAGAAATTCTAGTTACTTATAAATTCTTGGGA

CGGAAGCTTGGTACCAGATGTGGCTTTAGACAATAGGGAAGTGTCAATTCTGAATTGCTCA  
GATAAGGGGCTTTGCCTCCTGTTGGTCGACTTGATGGCCACCAGGTGATCTCTGGTCTCT  
TCAGTGTGGCTTTGCAGACTATAAAGGCGCAGCGCGCCAACGAGGCGGGTTGGCCCCAGA  
CGGCGGAGAGGAAGGGCAGAGTCGGCGGTCTGAGACTTGGGGCGGCCCCCTTGGAGGTCA  
GCCCCGCTCGCTCCTCCCGGCCCTCTCCTCCTCTCCGAGGTCCGAGGCGGGCAGCGGGCT  
GTGGGCGGGCAGGAGGTGCGGAGGGGCGGGGGCAGGAAGGGGCGGGGGGCTCGGCGCA  
CTCGGCAGGAAGAGACCGACCCGCCACCCGCCGTAGCCCGCGCGCCCCCTGGCACTCAATC  
CCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGCGCGTTCGGCCCCGGCT  
CTGGGGGCGCCAGGAACCTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCA  
GGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGAGACAGCTAACGGT  
GAGTTCCCGACCGACGGTCCGCTCCCCCGCAAGCCGACTGCCCCGGCTCTCCTGCCCCGT  
GGGGCGATCCCTCCCTAACACGCGGGCACACGCACACCCACGCACACTCACAGTCATGCA  
CACTACCCCGCACGCACACTCGCACTCACGCGCACACACGCGCGCGCACTCACACACAT  
TCACACACGCGCACACTTGCCTCACACGCGCGCGCATTACACGCATGCACACACACGC  
ACACTCACACGCGCGTGCAGCGCACACACAGTGCACGCGCGCGCACACTCACACTCACAGT  
GCACACACACATATACACTCACACTCCCTCAACTCCCTGCTGGGAGCAATGGCTGCTG  
ACTCGGCAGCCCCAGTTCCCTGCCAGACCTAGTCAGCAGTCCAGGACAGGCGCCAGTGG  
GATGCTGCCTCTTCCAAGCCCCAAACCTTCCCTTTTACCAAAGACAAAACAGGCCAGAA  
CTGGCAGGAGGGGAGACAGAGGGGAGAGAGCTCTCAAGGTGCAGAGCAAGACTGCGTAGG  
AGAGAGTTTGAAGGCGAGGGCTGGAGAGAAAGAACAAGGAAAGAGAGAGCCCCCTC  
GCTGAGGCTGCCGGGAGGATGGGGCAGAGCGGAGAGGAAGGCAGCCCGACCTCCAGCT  
TTCCAGATGTGGAATAGGAGAGGAGAGCGCAAGCGGAGGGCACTCAGGGGCTTCTAGAG  
GAGGCAAGTGGAGGAGGGTCTTGAAGGGTGATGTCCCGAGTCAGGGGAGTCTGGAGAGA  
GAGAGAGAGAGAGGGCTGCCAAGAAGGAAGCGCGGGCAAAGGCACAGGGGCACCAGATG  
CGGAAATGGGCAGCCTGTCTGGAGGCAGCTGTGGAGCTTCGATGGGTACCCCCAGCACC  
TGCCTGGGCAGAGCCTTGTGCTGAAGGGCCGGCGGGCAGGCCAGCCCTGAAAGCCTCGA  
CACCCAGGCAGACATGGATTCAGGACAGGCCATCTGAGCCCAGAGAGCAGACACAACAA  
TGGAAGCGGCACAGGGGTTTTGGGGCATGATGCTGAGTCTGGAGCTAAGAAAGCCTCCTT  
GGAAAGGCATCTGGGCTGAGATGCAAAGGAAGAATGGGAATTAGGTGAAAAATCAGAGG  
CGAGGGGTAGCATTACAGGGGAGGGGATAGCTAGTGCAGAGGCCCGGAGGTAAAGTGCCA  
GACTCAGCTCTTTGGAGCAACCGAACAGTTTCTAGAGGCTGGGTGCAGCTCTCCATTGGA  
TTAGAGGTTACAGGGGAGGCTGGCCAAGCATGTAGTTACATCAGGGAGGAGAAGGAGGA  
GCCAAGGAAGTGACTGGAGAGGCAGGTTGGGGTCAGATTGCAGGCCTTTGATGTCCTGTG  
AAGGCTGTTAGATCCTGGTGGTGTGGCCTGCTGTGGGCTCACATGTCTTCTTGGGCTGGC  
AGACCTTTCCATCCGGGGTTTTACCATTCTTCCCTTTCCCCATGCTGTGCCTCTCGGACC  
CCAAGGGACCTCAGAACAGCATGTCCGGATTTCAGTTCATCAAGAAGAAAAAGGTCATTAT  
GAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCACTGGTGACTGCCGGGCCCCCT  
TGTGACCCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGTACTTC  
CTCTCAGGGGCCCAGCCAGACTTGCAGCCCCTGGGGCACTTTACCAGCACAGCTCTTG  
GCCTCATGGGCACCGGCACGCCCCCTTGCTTGCCTAGCGCAGGAGCAACCTTAGGCTCAGC  
TTCCACCTGCCCTGGCTACCCTCCCTCTGGTCTGTCTCACTGTTCTATCCCCGCCCCA  
GGCTGTCCTCCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCC  
AGCAGCCAGTCTTTGGTCTTGGACCACACCGAGGACGGCTCAACATTAGGTGAGTAAT  
CCTGGCTCGGAGCCATGGTCTCAGGGTAGGGAAGGCAGCCCCCTGGGAGCTTCTCTCCTGC  
CTCCTCTCTGTCTTGGCCTGCCCCACTCTGTCCAAGTGGGCCTGACCACCATGTCTGTG  
TCTGCAGTCAGGCCTGGAGGACGGCGATCTATATGATGGAGCCTGGTGTGCTGAGGAGCA  
GGACGCCGATCCATGGTTTTAGGTGGACGCTGGGCACCCACCCGCTTCTCGGGTGTTAT  
CACACAGGGCAGGAACCTCTGTCTGGAGGTGAGGCAGACTAACCCTAGGTGAGGAGTAC  
AGAAGGACTGGGGTGGGAGTCTTGGGGGCACCGATGATCTCTCTCCACCTCTCCTGCCAG  
GTATGACTGGGTACATCATACAAGGTCCAGTTAGCAATGACAGTCGGACCTGGTGGGG  
AAGTAGGAACCACAGCAGTGGGATGGACGAGTGAAGTGGTCCCACTGTGGCTGGGGCCTC  
CATGCTGGGAGTTGGGCACCCAGTCCAGGCTAGGCTGAGGCTCCTCTGAGGACAAGGAAT

AGACGCCAGCTTAGGCTTCCCAGGGGGGTGTGGCTTGTGTCAAGAGGGTGGCACACGGC  
 AGGCACCATTGGGAGCCAGCTGCTTTGGGACATGCCCACATCCTCCCCAGATAATGCCAC  
 CACAGGGTGGGTGCTGCTTACGGTACAGCTTCTCCTGGCGTGCCCTTCTGGCCCCGG  
 GCCTCTGGTCCACATCACTTCTTGCCTTCTCGTGGTTCTGACTTCCGCATCTCATGGACC  
 TCTTTTTACAGCAGGCTACAATGTGGAGTCTGGCCAGCTCTAGGATTGGCTTCCCCGA  
 GTCATGTGGCCAACTGGTCTAATGAACTGTGTCCAATCCAGAGAGCAAGGCTGCCTAGG  
 GCTGCCCATTGGCAGGGGGCTGTGGGCCGGGGTCTGTGTTTGATGCACAGTGCAAGTCTCT  
 AGCTGAGCCCACTAGGGTGGGGAGACAGTAAGCTTGGAGGCCTGAGCTCCTTCCCTGGGT  
 CCTGGGCCAGGCTTCTGGGGTTTGAGCAGCCACAACAGAGAACTTGCTGCCCCCAGGTAT  
 TTCCTGCCAATTCCAGACCCAGAACTCCAGTGCTGAACCTCCTGCCGAGCCCCAGGTGG  
 CCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGCGCGCTTGCCTCCGGG  
 CAGAGATCCTGGCCTGCCAGTCTCAGGTGGGCAGTCAGGCCAGGGTTGGTTGGGCAGGG  
 CTTGGATGCAGGGTGCATCCTTCACTGTGGACACACCCTTTACCATAAACTCAACCTCCA  
 CCAGACCCCAATGACCTATTCTTTGAGGCCCTGCGTCGGGATCCTCTGACCCTCTAGAC  
 TTTTCAGCATCACAATTACAAGGCCATGAGGAAGGTGAGATATAACCCCTATGACCTGGGA  
 AGGAGGGCCCCACCCATCTCAGGTCCCCTTCCCACCTTCCCACCGGGGCACAACCTGCTGT  
 GACTGCGCTTGTATGCCCCCTGCTGCCTCCTGATGTCTCAGCCTTCTCTCCTGTGGACCCC  
 TAAGCTCCATCCCCTTTCCCTTATTATGGCGCCCCCCCCAGTCTTACCCCTTCTTCCCGG  
 CTCTGCTGCCGCTCCCCTCCTGTACCATGATGGGATGCCCCCTCTGTGTGGGCCATCGCT  
 GACTTTTTAAGTCTTTCCATGGCACATGTGATCTGCCCTGGGTGTACCCCTCCCATGCC  
 TCATGCCACGCTACACTCTGCCACCAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA  
 CATCACCCGCATCTACAGCATTTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA  
 AATGTCCGACAAGCCTGGGGAGCATGAGCTGGGTACTGGCATGGGGAGTGGGGAGAGGTA  
 GGCACAGGGCAGGGCCCCAGGCATGAACCCGCTGCAAGCCCCCATGTGTCCCCAGGGGAG  
 CCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTT  
 CTGCTCCTGATGCAGTTCTGTGCCATGAGTTCTTGCAGGGGAACCCACGGGTGACCCGG  
 CTGCTCTCTGAGATGCGCATTCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC  
 GCCTACCACCGGGTAGGCCACCCAGCATGAGGGCCACTCTGTCTTCTGCCCTGGTGGCT  
 GGACCTGCTCGACTTGAACAAGCCTCTTGCCCGGCAGGGTTTCCAGAGCTGGTGGGCTGGGC  
 CGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTCAACAC  
 ACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCATCACCT  
 GCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGAGTATTTTGAGGGCGGCAGT  
 GGAGGTCTGTGGGGGGCGGACCTTGTCTCTGTCTCCTGCCCCCTCCTGACCTGCCCCATCC  
 AGGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAA  
 GTGCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTTCGACATGACTCGCACCC  
 CGTGGGCTGCCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCA  
 CTGTCTATGCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCCTGCCACAGCC  
 AGGACTTCTCCGTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGA  
 GTATGTGCCTGAGGGTGGAGTTAGCCCTGGCCCCGTAACCCCGCCCTGATAAGACAGCC  
 TGCGGTTGCGTACAGTGCTGGCGTCTGTTCCCACTCTGAAGTGTCCCTCAGAGAAGGGAG  
 GGTAGCGGGAGGATGGGACCGCATCCCGCCTGCTTAGGCAGCAGTGTCTGTGGTCCCCTT  
 AGGCATGAATGACTTCAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTC  
 CTGTGACAAGTTCCCTCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGC  
 CCTCCTCACCTACCTGGAGCAGGTGGATCTGCGTCCCGGCCCCAGCCTGCCTGAATCA  
 CTCCTGCTGTCCATTTAGGCTACAGCTCCTACCAGGGGTCTTCTAAGGTCCAGCTGAGC  
 ATTCAGACTCACAAGATGCCATGGGCCATGCTTGGTATCAGATTGTCTTGGAAGCACACA  
 GGACAGGAAGTGAGTTTGCTGGCAGCGTGGCATCGTGTTAGAGCCGGTGGGAGGAGCCT  
 CCATTGCAGTCTAGGTGGTGGTCCGTGGCGTGGCCCCAGAGCTATCCTCAGGAGAGACTC  
 ACGTGAGGCAGGTGCAGGAGCTGTCTGGCATAGAAGCTTCATGTTCCATGGAGCTCATA  
 ACCCTTGTAATAGCTCCATAAGCAGAGCTTCCAAAGGGTCTACCAAAGACAAGCCCAATA  
 ACCTGGGAAAGCCCAAGGATAGATAAGCCTTCTTACCAGGTATTTATCATTTTCTTAGTC  
 CAGATGTGATTTGTCAATCAGGATTTCTTTTTTTTTTTTCTTCCAGAAGTAGTGTACCT

AGGAACACAGTAGACCTACCACTTTGCTCAGGTTTGCAGGGCAACAGAGCCAGCAAGTTA  
GCTAAACAGCACATTATCCTGCCGAAGGGGAAGGGCTCTGATAACCTCTTCCCACACAGG  
TGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACG  
CTGTCAATTGCCGTGGATGGGATTAACCATGACGTGACCACGGGTGTGTTTGACCGGGAGG  
GCAAGGGAAGGGGCTGGAGGGCTGGAGGCTCGGGAAGAAGCAGAAGATCATTAAATTGGGT  
CCTGATCGTGCCTTCACTCTCCTCAGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCC  
CAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACGTGTC  
GGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTCTGTGCTCACCAAGACTCCCAAAC  
AGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCC  
TGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCT  
GGACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTG  
CTCATTAAAGCTACCGGGCACCTTAGCTCATCTTCGTGTTGTCTCTGTGCCCCAGGTCCT  
CCCCCGGGGGCGGGCCTCGGCCAGCCCTCAGTTCCTATTCTGCACACTTGCACACTCT  
CATCAGTTGGCTTCTGGACACATTGTGTGAAAAGAGGATCCCACCTGGGCTCTTCTTGAA  
CCAAGGGCCTGGCAGAGCAACTCATTTCTTCTGATCAGCTTCTGCTACAGGTACCATTAC  
ACTGCTGCCAGGCATTCTGTAAGCGCCTGCTCATTGCCAGGTGTGCAAGGAATCAGGATC  
AGCCGTGCCTGCACTCAAACCTCCTGGGGCTCCTAGTCAAGGGAAAGGACAGTTCGGTACA  
TTGTGAGACATGCTAGGGTGGAGGCCAGGTGCCGTGAGAGTGCAGGGGAGCTGCACACGT  
GAAATACAGCACTGCACATCAACAGGACTGGGGCAGTCAAGGATGCAATAGAAGTAGTGG  
CTCTAGAAGTTCAGGCGGGAGGTGGGCAGGGTGTGGAGTATGGACAGGGATGGCTCCAAG  
GAGGAGGGTCAGCCAAAGGTGGGTGAGCTGAGAACATTTGAATTTGCTTCAGCCATTCTC  
AGAGTATTGATAACTGATAGGCTTTGCTGAGTTTCTATCAGACTGAAGGGGAAGTTGTGT  
ATCAGTCTGTGTCTTGCCAGGTAAACAACCCATTCTAGGCACTTAAAGTGAGGGAAATT  
TAATGCTGGAAATTGGATAGGAAGGTGTTGGAAGAGCTGGATGAGGCCGGGTGTGGTGGC  
TCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGA  
GTTTGAGACCAGCCTGGATAACATAGCCAAACCCCGCCTCTACAAAATAAGAAATAAGA  
AACATAGCCAGCTGTAGTGGCGCATGGCTAAGGGAGGCAGAGGCAGGAGGATCACTGGAG  
CCTGGGAGGTGGAGGCTGCAGAGGCAGCAGTGAGCCATGATGGCGCCACTATACTCCAAC  
CTGGATGGTCATAACAAAATAAACAACAAAAA (SEQ ID NO:3)

FIG 9

>CG54007-04  
**ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG** 60  
 GCGCCAGGAACCTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120  
 ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGAGACAGCTAACGGGACCTCA 180  
 GAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240  
 AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCCTTGTGACCCCACT 300  
 CCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360  
 GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420  
 GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480  
 GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540  
 CCCACCCGCTTCTCGGGTGTATCACACAGGGCAGGAACCTCTGTCTGGAGGTATGACTGG 600  
 GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC 660  
 CACAGCAGTGGGATGGACGCAGTATTTCTGCCAATTTCAGACCCAGAACTCCAGTGCTG 720  
 AACCTCCTGCCGAGCCCCAGGTGGCCCGCTTCATTTCGCTGCTGCCCCAGACCTGGCTC 780  
 CAGGGAGGCGCGCTTGCCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAAT 840  
 GACCTATTCTTTCAGGCCCCCTGCGTCGGGATCCTCTGACCTCTAGACTTTTCAGCATCAC 900  
 AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC 960  
 CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCTG 1020  
 GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT 1080  
 GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG 1140  
 TTCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTACCTGCTG 1200  
 CCCTCCATGAACCTGATGGCTATGAGATCGCCTACCACCGGGGTTTCAGAGCTGGTGGGC 1260  
 TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC 1320  
 AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT 1380  
 CACCTGCCATTGCCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG 1440  
 GCAGTAATCAAGTGGATGAAGCGGATCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT 1500  
 GAGCTCGTGGTGTCTACCCATTTCGACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA 1560  
 GTGACACGGAACGTGCGGGTCACCTTTGAAGAGGGCCCCCTCCCTGCAATTTTCGTGCTC 1620  
 ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG 1680  
 GACCTTCGAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGAT**TGA** (SEQ ID NO:5) 1725

FIG. 10

>CG54007-04  
 MWGLLLALAAFAVAPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60  
 EQHVRIIRVIKKKVIMKKRKLTLTRPTPLVTAGPLVPTPAGTLDPAEKQETGCPPLGL 120  
 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180  
 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240  
 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300  
 NYKAMRKLKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360  
 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYHRGSELVG 420  
 WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVP HIVPNHHLPLPTYTLPNATVAPETR 480  
 AVIKWMKRIPFVLSANLHGGELVVSYPFDMVTASAEGYHSVTRNCRVTFEEGPFPCNFVL 540  
 TKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD (SEQ ID NO:6) 574

FIG. 11

>CG54007-05

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ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCCGGCTCTGGGG 60
GCGCCACAGGAACCTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGGAGACAGCTAACGGGACCTCA 180
GAACAGCATGTCCGGATTTCAGTGCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCCTTGTGACCCCACT 300
CCAGCAGGGACCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGAGATCCTGGCCTGCCAGTCTCAGA 600
CCCCAATGACCTATTCTTGAGGCCCCCTGCGTCGGGATCCTCTGACCCCTCTAGACTTTCA 660
GCATCACAAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA 720
CATCACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA 780
AATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGG 840
CATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTG 900
CCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCA 960
CCTGCTGCCCTCCATGAACCTGATGGCTATGAGATCGCCTACCACCGGGGTTTCAGAGCT 1020
GGTGGGCTGGGCGGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGC 1080
TGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCC 1140
CAACCATCACCTGCCATTGCCCACCTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGA 1200
AACGCGGGCAGTAATCAAGTGATGAAGCGGATCCCCCTTTGTGCTAAGTGCCAACCTCCA 1260
CGGGGGTGAGCTCGTGGTGTCTTACCCATTTCGACATGACTCGCACCCCGTGGGCTGCCCCG 1320
CGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGG 1380
CAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGT 1440
GCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTT 1500
CAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCC 1560
TCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAGACGCCCTCCTCACCTACCT 1620
GGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGAT 1680
TGCTGACGCTGTCTATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGG 1740
GGATTATTGGCGTCTGCTGACCCACAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTA 1800
CCATTTCAGTGACACGGAACGTGTCGGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTT 1860
CGTGCTCACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGT 1920
GCCCCCGGACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:7) 1972

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FIG. 12

>CG54007-05

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MWGLLLLALAAFAVAPVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
EQHVRIRVIKKKKVIMKKRKLTLTRPTPLVTAGPLVPTPAGTLDPAEKQETGCPPLGL 120
ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGLYDGAWCAEEQDADPWFQVDAGH 180
PTRFSGVITQGRDPGLPSLRPQ (SEQ ID NO:8) 202

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FIG. 13

>CG54007-06

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ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG      60
GCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG      120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGGAGACAGCTAACGGGACCTCA      180
GAACAGCATGTCCGATTTCGTGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG      240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCCTTGTGACCCCACT      300
CCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG      360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT      420
GGACCACACCGAGGACGGCTCAACATTTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT      480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC      540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG      600
GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC      660
CACAGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTG      720
AACCTCCTGCCGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTC      780
CAGGGAGGCGCGCTTGCCCTCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAAT      840
GACCTATTCTTGTAGGCCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTTCAGCATCAC      900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC      960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTG      1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT      1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCTGTGCCATGAG      1140
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG      1200
CCCTCCATGAACCTGATGGCTATGAGATCGCTTACCACCGGGGTTTCAGAGCTGGTGGGC      1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC      1320
AACACACCACGTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT      1380
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG      1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT      1500
GAGCTCGTGGTGTCTTACCCATTGACATGACTCGCACCCCGTGGGCTGCCCGCGAGCTC      1560
ACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAAT      1620
CTGGCCATGCAGGACACCAGCCGCCGACCCCTGCCACAGCCAGGACTTCTCCGTGCACGGC      1680
AACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTCAGCTAC      1740
CTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCCTCACGAG      1800
AATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG      1860
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGAC      1920
GCTGTCAATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTAT      1980
TGGCGTCTGCTGACCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA      2040
GTGACACGGAAGTGTGGGTACCTTTGAAGAGGGCCCCCTCCCTGCAATTTCTGTGCTC      2100
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG      2160
GACCTTCGAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:4)      2205

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CG54007-06

SECRET

Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 510/510 (100%), Positives = 510/510 (100%)

Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0  
Identities = 67/69 (97%), Positives = 67/69 (97%)

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Query:      507 PFD-MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 565
            P D MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR
Sbjct:     666 PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 725

Query:      566 LERLRGQKD 574 (SEQ ID NO:6)
            LERLRGQKD (SEQ ID NO:41)
Sbjct:     726 LERLRGQKD 734 (SEQ ID NO:42)

```

Figure 15

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE  
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.  
Length = 734

Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101  
Identities = 192/193 (99%), Positives = 193/193 (100%)

Query: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGETTKVPGSTPALHSSPAQPPAETANGTS 60  
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGETTKVPGSTPALHSSPAQPPAETANGTS  
Sbjct: 1 MWGLLLALAAFAVGPALGAPRNSVLGLAQPGETTKVPGSTPALHSSPAQPPAETANGTS 60

Query: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120  
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL  
Sbjct: 61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPPTAGTLDPAEKQETGCPPLGL 120

Query: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180  
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH  
Sbjct: 121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query: 181 PTRFSGVITQGRD 193 (SEQ ID NO:8)  
PTRFSGVITQGR+ (SEQ ID NO:43)  
Sbjct: 181 PTRFSGVITQGRN 193 (SEQ ID NO:44)

TOGETHER "STRESS"

Figure 16

>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE  
METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.  
Length = 734

Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0  
Identities = 734/734 (100%), Positives = 734/734 (100%)

```

Query:      1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:      1 MWGLLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:     61 EQHVIRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVIRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:     61 EQHVIRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:    121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:    121 ESLRVSDSRLEASSSQSFGLGPHRGRNLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDETPV 240
             PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDETPV
Sbjct:    181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTTWGSRNHSSGMDAVFPANSDETPV 240

Query:    241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
             NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:    241 NLLPEPQVARFIRLLPQTLWQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:    301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360
             NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH
Sbjct:    301 NYKAMRKLKMQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH 360

Query:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420
             GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG
Sbjct:    361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG 420

Query:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480
             WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR
Sbjct:    421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTTLPNATVAPETR 480

Query:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTDDAVFRWLSTVYAGSN 540
             AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTDDAVFRWLSTVYAGSN
Sbjct:    481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTDDAVFRWLSTVYAGSN 540

Query:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
             LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct:    541 LAMQDTSRRPCHSQDFS VHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660
             NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
Sbjct:    601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Query:    661 WRLLT PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
             WRLLT PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct:    661 WRLLT PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query:    721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
             DLRRRLERLRGQKD (SEQ ID NO:45)
Sbjct:    721 DLRRRLERLRGQKD 734 (SEQ ID NO:46)

```

[illegible]

**kDa**

98

66

55

36

30

21

16

6

**KKLTLTRPTPLVTAGPL**

|||||

**KKLTLTRPPPLV-AGPL**

Figure 18 ClustalW alignment of CG54007-01, CG54007-04 and CG54007-05 proteins of the present invention.

```

CG54007-05 MWGLLL LALA AFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAOPPAETANGTS
CG54007_01 MWGLLL LALA AFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAOPPAETANGTS
CG54007-04 MWGLLL LALA AFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAOPPAETANGTS

CG54007-05 EQHVRIRV I KKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007_01 EQHVRIRV I KKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007-04 EQHVRIRV I KKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL

CG54007-05 ESLRVSDSRLEASSSQSFG LGPHRGRLNIQSGLEDGDL YDGAWCAEEQDADPWFOVDAGH
CG54007_01 ESLRVSDSRLEASSSQSFG LGPHRGRLNIQSGLEDGDL YDGAWCAEEQDADPWFOVDAGH
CG54007-04 ESLRVSDSRLEASSSQSFG LGPHRGRLNIQSGLEDGDL YDGAWCAEEQDADPWFOVDAGH

CG54007-05 PTRFSGVITQGRD-----PGLP SLRPQ-----
CG54007_01 PTRFSGVITQGRNSVWR YDWWTSYKVQFSNDSRTWWGSRNHS SGMDAVFPANSDPETPVL
CG54007-04 PTRFSGVITQGRNSVWR YDWWTSYKVQFSNDSRTWWGSRNHS SGMDAVFPANSDPETPVL

CG54007-05 -----
CG54007_01 NLLPEPQVARFIRLLPQTWLOGGAPCLRAEILACP VSDPNDLFLEAPASGSSDPLDFQHH
CG54007-04 NLLPEPQVARFIRLLPQTWLOGGAPCLRAEILACP VSDPNDLFLEAPASGSSDPLDFQHH

CG54007-05 -----
CG54007_01 NYKAMRKLMKQVQEQC PNI TRIYSIGKSYQGLKLYV MEMSDKPGEHELGEPEVRYVAGMH
CG54007-04 NYKAMRKLMKQVQEQC PNI TRIYSIGKSYQGLKLYV MEMSDKPGEHELGEPEVRYVAGMH

CG54007-05 -----
CG54007_01 GNEALGRELL LLLMQFLCHEFLRG NPRVTRLLSEMR IHL LPSMNP DGVEIAYHRGSELVG
CG54007-04 GNEALGRELL LLLMQFLCHEFLRG NPRVTRLLSEMR IHL LPSMNP DGVEIAYHRGSELVG

CG54007-05 -----
CG54007_01 WAEGRWNNQSIDLNHN FADLNTPLWEAQDDGKVPH I V PNHHLPLPTVYTLPNATVAPETR
CG54007-04 WAEGRWNNQSIDLNHN FADLNTPLWEAQDDGKVPH I V PNHHLPLPTVYTLPNATVAPETR

CG54007-05 -----
CG54007_01 AVIKWMKR I PFWLSANLHG GELVVSYPFDMTRTPWAAARELTPTPDDAVFRWLSTVYAGSN
CG54007-04 AVIKWMKR I PFWLSANLHG GELVVSYPFDMV-----

CG54007-05 -----
CG54007_01 LAMQDTSRRPCHS QDFSVHGNI INGADWHTVPGSMNDFS YLHTNCFEVTVELSCDKFPHE
CG54007-04 -----

CG54007-05 -----
CG54007_01 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTE LGIADAV IAVDGINHDVTTAWGGDY
CG54007-04 -----TAS-----

CG54007-05 -----
CG54007_01 WRLLTPGDYMTAS AEGYHSVTRNCRVTFEEGFPFCNFVLT KTFKQRLRELLAAGAKVFP
CG54007-04 -----AEGYHSVTRNCRVTFEEGFPFCNFVLT KTFKQRLRELLAAGAKVFP

CG54007-05 -----
CG54007_01 DLRRRLERL RGQKD
CG54007-04 DLRRRLERL RGQKD

```

Fig.19

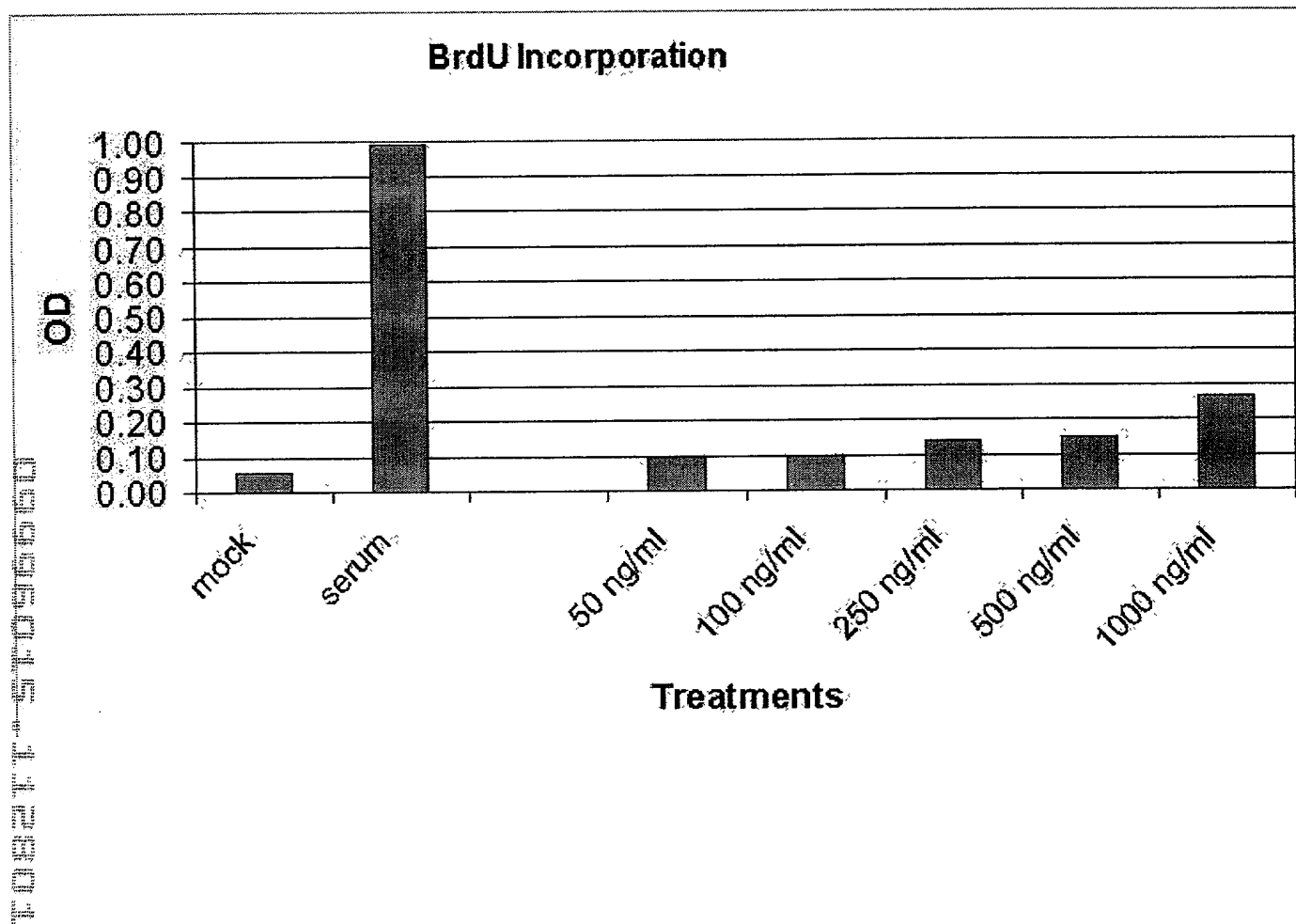


Fig. 20

